Integrative Cancer Research Special Interest Group Teleconference

Pathways SIG Meeting Minutes

Date, Time & Location:	October 5, 2004 1:00 – 2:00 PM EDT		
Attendees:	**First Name**	**Last Name**	**Institution**
	Gary	Bader	MSKCC
	Brian	Gilman	Panther Informatics
	David	Jewell	Dartmouth Norris Cotton Cancer Center
	Michael	Keller	Booz Allen Hamilton
	Juli	Klemm	3rd Millennium
	Shannon	McWeeney	OHSU
	Tom	Moloshok	Fox Chase Cancer Center
	John	Rux	The Wistar Institute
	Carl	Schaefer	NCICB
	Craig	Street	Penn
Review Discussions from last meeting:	**Introduce New SIG Lead** - Shannon McWeeney is the new lead for this SIG. Shannon is an Assistant Professor of Bioinformatics and Biostatistics at OHSU and will be an adopter for the MSKCC Pathways project and the UCSF QPACA project. **Update on Use Cases** - The caGRID team is conducting interviews with ICR participants who submitted use cases in order to map these requirements to the grid architecture that is being defined. Their initial findings will be presented at this month's ICR WS teleconference **Update on project-level and SIG-level support from the cross-cutting workspaces** - The leads for the cross-cutting workspaces have been identifying facilitators to provide SIG-level and project-level support. Quan Chen (**quchen@aecom.yu.edu**) will be the facilitator for VCDE for this SIG. Project-level support will be provided from the Architecture group and those pairings should be available within a week.		
Cytoscape Presentation:	Gary Bader gave a Centra presentation of Cytoscape. The slides can be found at: http://cabig.nci.nih.gov/workspaces/ICR/Meetings/SIGs/Pathways/20041005_Cytoscape_presentation/file_view <u>Questions and Comments regarding the presentation:</u> John Rux: Q: What is the source of the protein-protein interaction data? A: Cytoscape as plugins for loading cPath and BIND data. Other data is input through an Excel-like upload Juli Klemm Q: Do you know how many Cytoscape users there are? How do you		

prioritize the requirements for new releases?

A: For Cytoscape 2.0, there have been about 1600 downloads and about 60% of them are unique. To prioritize features for releases, there are regular Cytoscape retreats involving about 40 people, where this is discussed.

Juli Klemm Q: Do the edges in a Cytoscape representation have meaning:

A: Not in any canonical way – only as the user defines them. May support styles in the future.

John Rux Q: How are the different states of a protein represented, e.g. phosphorylated vs nonphosphorylated protein?

A: This is entirely up to the user at this point.

Brian Gilman Q: Can Cytoscape represent the concept of state of a sample? For example, I may want to grow yeast in two different media, they overlay the expression results on a pathway of interest.

A: Yes, we can overlay multiple experiments simultaneously on a network.

Brian Gilman Q: Is it possible to detect/view correlations between nodes in a set of states?

A: This is difficult in Cytoscape 2.0. In 1.1, there was an expression data viewer plugin where you could select a node, then use a slider bar to look for correlations between selected nodes.

Brian Gilman Q: Is there an algorithm for Cytoscape to define hubs?

A: One can rank the network by node degree: # connections/node. But, no real "hub finding" plugin.

Action Items:	Name Responsible	Action Item	Date Due	Notes
	Juli Klemm	Post materials on the caBIG website		
	Juli Klemm	Distribute meeting minutes		